



NREL Seq listing 399697  
SEQUENCE LISTING

<110> NATIONAL RENEWABLE ENERGY LABORATORY  
Himmel, Michael E.  
Adney, William

<120> ENDOGLUCANASE MUTANTS AND MUTANT HYDROLYTIC DEPOLYMERIZING  
ENZYMES AND USES THEREOF

<130> NREL 99-38

<140> US 09/997,504  
<141> 2001-11-19

<150> US 60/134,925  
<151> 1999-05-19

<160> 14

<170> PatentIn version 3.2

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<213> Acidothermus cellulolyticus

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ctctggtcac gcgactaccg cagcatgctc gaccagataa agtcgctcgg ctacaacaca 180  
atccggctgc cgtactctga cgacattctc aagccgggca ccatgccgaa cagcatcaat 240  
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 <213> Acidothermus cellulolyticus

<220>  
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Asn Asn Val Pro Val Arg Ile Ala Gly Ile Asn Trp Phe Gly Phe Glu  
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Thr Cys Asn Tyr Val Val His Gly Leu Trp Ser Arg Asp Tyr Arg Ser  
 35 40 45

Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn Thr Ile Arg Leu Pro  
 50 55 60

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Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met Pro Asn Ser Ile Asn  
 65 70 75 80  
 Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu Thr Ser Leu Gln Val  
 85 90 95  
 Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile Gly Leu Arg Ile Ile  
 100 105 110  
 Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln Ser Ala Leu Trp Tyr  
 115 120 125  
 Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser Asp Leu Gln Ala Leu  
 130 135 140  
 Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val Gly Phe Asp Leu His  
 145 150 155 160  
 Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys Gly Asp Pro Ser Ile  
 165 170 175  
 Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn Ala Val Leu Ser Val  
 180 185 190  
 Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val Gln Ser Tyr Asn Gly  
 195 200 205  
 Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly Ala Gly Gln Tyr Pro  
 210 215 220  
 Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr Ser Ala His Asp Tyr  
 225 230 235 240  
 Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser Asp Pro Thr Phe Pro  
 245 250 255  
 Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp Gly Tyr Leu Phe Asn  
 260 265 270  
 Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe Gly Thr Thr Leu Gln  
 275 280 285  
 Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu Val Gln Tyr Leu Arg  
 290 295 300

Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln Trp Thr Phe Trp Ser  
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305 310 315 320

Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile Leu Lys Asp Asp Trp  
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Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu Ala Pro Ile Lys Ser  
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Ser Ile Phe Asp Pro Val Gly  
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<210> 9  
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<212> DNA  
<213> Acidothermus cellulolyticus

<220>  
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<223> DNA sequence for Y245G Mutant SEQ ID: 9

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ctctggtcac gcgactaccg cagcatgctc gaccagataa agtcgctcgg ctacaacaca 180  
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agcgggcagt cggcgctgtg gtacacgagc agcgtctcgg aggctacgtg gatttccgac 420  
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tactgtctacg cccacgcccc cggcaagccc gacgccgtca ccgacggcag cctccggagc 1260  
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<211> 358  
<212> PRT  
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<220>  
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1 5 10 15

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20 25 30

Thr Cys Asn Tyr Val Val His Gly Leu Trp Ser Arg Asp Tyr Arg Ser  
35 40 45

Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn Thr Ile Arg Leu Pro  
50 55 60

Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met Pro Asn Ser Ile Asn  
65 70 75 80

Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu Thr Ser Leu Gln Val  
85 90 95

Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile Gly Leu Arg Ile Ile  
100 105 110

Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln Ser Ala Leu Trp Tyr  
115 120 125

Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser Asp Leu Gln Ala Leu  
130 135 140

Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val Gly Phe Asp Leu His  
145 150 155 160

Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys Gly Asp Pro Ser Ile  
165 170 175

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Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn Ala Val Leu Ser Val  
180 185 190

Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val Gln Ser Tyr Asn Gly  
195 200 205

Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly Ala Gly Gln Tyr Pro  
210 215 220

Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr Ser Ala His Asp Tyr  
225 230 235 240

Ala Thr Ser Val Gly Pro Gln Thr Trp Phe Ser Asp Pro Thr Phe Pro  
245 250 255

Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp Gly Tyr Leu Phe Asn  
260 265 270

Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe Gly Thr Thr Leu Gln  
275 280 285

Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu Val Gln Tyr Leu Arg  
290 295 300

Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln Trp Thr Phe Trp Ser  
305 310 315 320

Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile Leu Lys Asp Asp Trp  
325 330 335

Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu Ala Pro Ile Lys Ser  
340 345 350

Ser Ile Phe Asp Pro Val  
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<210> 11  
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<212> DNA  
<213> Acidothermus cellulolyticus

<220>  
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 <213> Acidothermus cellulolyticus

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Thr Cys Asn Tyr Val Val His Gly Leu Arg Ser Arg Asp Tyr Arg Ser  
35 40 45

Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn Thr Ile Arg Leu Pro  
50 55 60

Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met Pro Asn Ser Ile Asn  
65 70 75 80

Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu Thr Ser Leu Gln Val  
85 90 95

Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile Gly Leu Arg Ile Ile  
100 105 110

Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln Ser Ala Leu Trp Tyr  
115 120 125

Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser Asp Leu Gln Ala Leu  
130 135 140

Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val Gly Phe Asp Leu His  
145 150 155 160

Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys Gly Asp Pro Ser Ile  
165 170 175

Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn Ala Val Leu Ser Val  
180 185 190

Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val Gln Ser Tyr Asn Gly  
195 200 205

Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly Ala Gly Gln Tyr Pro  
210 215 220

Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr Ser Ala His Asp Tyr  
225 230 235 240

Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser Asp Pro Thr Phe Pro  
245 250 255

Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp Gly Tyr Leu Phe Asn  
260 265 270

Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe Gly Thr Thr Leu Gln  
275 280 285

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Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu Val Gln Tyr Leu Arg  
290 295 300

Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln Trp Thr Phe Trp Ser  
305 310 315 320

Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile Leu Lys Asp Asp Trp  
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Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu Ala Pro Ile Lys Ser  
340 345 350

Ser Ile Phe Asp Pro Val  
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<210> 13  
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<212> DNA  
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 <213> Acidothermus cellulolyticus

<220>  
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 20 25 30  
 Thr Cys Asn Tyr Val Val His Gly Leu Trp Ser Arg Asp Tyr Arg Ser  
 35 40 45  
 Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn Thr Ile Arg Leu Pro  
 50 55 60  
 Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met Pro Asn Ser Ile Asn  
 65 70 75 80  
 Phe Arg Gln Met Asn Gln Asp Leu Gln Gly Leu Thr Ser Leu Gln Val  
 85 90 95  
 Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile Gly Leu Arg Ile Ile  
 100 105 110  
 Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln Ser Ala Leu Trp Tyr  
 115 120 125  
 Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser Asp Leu Gln Ala Leu  
 130 135 140

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Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val Gly Phe Asp Leu His  
145 150 155 160

Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys Gly Asp Pro Ser Ile  
165 170 175

Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn Ala Val Leu Ser Val  
180 185 190

Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val Gln Ser Tyr Asn Gly  
195 200 205

Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly Ala Gly Gln Tyr Pro  
210 215 220

Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr Ser Ala His Asp Tyr  
225 230 235 240

Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser Asp Pro Thr Phe Pro  
245 250 255

Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp Gly Tyr Leu Phe Asn  
260 265 270

Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe Gly Thr Thr Leu Gln  
275 280 285

Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu Val Gln Tyr Leu Arg  
290 295 300

Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln Trp Thr Phe Trp Ser  
305 310 315 320

Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile Leu Lys Asp Asp Trp  
325 330 335

Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu Ala Pro Ile Lys Ser  
340 345 350

Ser Ile Phe Asp Pro Val  
355